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CAGCGTCAGACGCAGGGCACTGAGAATGTGCGACAGCGCGCAACGATGAAGTAGCCCAGAGGGTCCCTTG  
 GAAAATGAGGCCAGGGTCCCTGCTGCTGCTGTTCTGCTGCTCGCCCTGTCAGGAGCCTGCGGGGCAAA  
 GAGTGTGCGTCTCCACCCTGTGAGTGTACCAGGAGGACGACTTCAGAGTCACCTGCAAGGAGCTCCACC  
 GAATCCCCAGCCTGCCGCCCAGCACCCAGACTCTGAAGCTCATCGAGACTCATCTGAAGACCATAACCCAG  
 TCTTGCAATTTTCGAGTCTGCCCCAATATTTCCAGGATCTATTTATCTATAGATGCAACTCTGCAGCGGCTG  
 GAACCACATTTCTTCTACAATTTGAGTAAATGACTCACATAGAAATCCGGAACACCAGAAGCTTAACCT  
 ATATAGACCCTGATGCGCTTGACAGAGCTCCCTTGCTCAAGTTTCTTGGCATTTTCAATACTGGACTTAG  
 AATATTTCCCTGACTTGACCAAAATTTATTTCCACGGACATATTCTTTATACTTGAAATCACAGACAACCCCT  
 TACATGACTTCGGTCCCTGAAAACGCATTCAGGGCCCTATGCAATGAAACCTTGACCCTGAAACTGTACA  
 ACAATGGATTTACTTCAGTCCAAGGACATGCTTTCAATGGAACAAAGCTGGATGCTGTTTACCTAAACAA  
 GAATAAATACCTGACAGCTATAGACAACGATGCTTTTGAGGAGTATACAGTGGACCAACTTTGCTAGAT  
 GTGTCTTCCACCAGCGTCACTGCCCTTCCTTCCAAAGGCCCTGGAGCACCTCAAAGAACTGATCGCAAAAG  
 ACACCTGGACTCTCAAAAAGCTCCCGCTGTCGTTGAGTTTCCCTCCACCTCACTCGGGCTGACCTCTCTTA  
 CCCGAGCCACTGCTGCGCTTTTAAGAACCAGAGAAAATCAGGGGAATCCTGGAGTCTTTGATGTGTAAT  
 GAGAGCAGTATCCGGAACCTTCGTCAAAGGAAATCAGTGAACATCTTGAGGGGTCCCATCTACCAGGAAT  
 ATGAAGAAGATCCGGGTGACAACAGTGTGGGTACAAACAAAACCTCCAAGTTCCAGGAGAGCCCAAGCAA  
 CTCTCACTATTACGTCTTCTTTGAAGAACAAGAGGATGAGGTCGTTGGTTTCGGCCAAGAGCTCAAAAAT  
 CCTCAGGAAGAGACTCTCCAAGCCTTCGAGAGCCACTATGACTACACGGTGTGTGGGGACAACGAGGACA  
 TGGTGTGTACCCCCAAGTCGGACGAGTTTAACCCCTGTGAAGATATCATGGGCTACAGGTTCCCTGAGAAT  
 CGTGGTGTGGTTTGTGAGTCTGCTGGCTCTCCTGGGCAATATCTTCGTCCCTGCTCATTTCTGCTAACCCAGC  
 CACTACAAATTGACCGTGCCGCGGTTCCCTCATGTGCAACTTGGCCTTTGCAGATTTCTGTCATGGGGGTAT  
 ACCTGCTTCTCATTTGCTCTGTAGACCTGTACACACACTCTGAGTACTACAACCACGCCATCGACTGGCA  
 GACGGGCCCCGGGTGCAACACGGCTGGCTTCTTCACTGTTTTCGCCAGTGAGTTATCAGTGTACACACTG  
 ACGGTCATCACCTGGAGCGATGGTACGCCATCACCTTCGCCATGCGCCTGGATAGGGAAGATCCGCTCA  
 GGCACGCGTACACCATCATGGCTGGGGGCTGGGTTTCTGCTTCCCTTCTCGCCCTGCTCCCCGATGGTGGG  
 AATCAGCAGCTATGCCAAGGTCAGCATCTGCCTGCCAATGGACACCGACACCCCTCTTGCACTCGCATAC  
 ATTGTCTCGTTCTGCTGCTCAATGTTGTTGCCCTTTGTTGTCGTCTGTTCCCTGCTATGTGAAGATCTACA  
 TCACGGTCCGAAATCCCCAGTACAACCCCTCGAGATAAAGACACCAAGATTGCCAAGAGGATGGCTGTGTT  
 GATCTTCACTGACTTCATGTGCATGGCGCCCATCTCCTTCTATGCGCTGTGCGCACTTATGAACAAGCCT  
 CTAATCACTGTTACTAACTCCAAAATCTTGTTGGTTCTCTTCTACCCCTCAACTCCTGTGCCAATCCGT  
 TTCTCTATGCTATTTTACCAAGGCCTTCCAGAGGGACGTGTTTCATCTGCTCAGCAAGTTTGGCATCTG  
 CAAACGCCAGGCCAGGCCTATCAGGGTCAGAGAGTCTGTCCCAACAATAGCACTGGTATTCAGATCCAA  
 AAGATTCCCCAGGACACGAGCGAGAGTCTCCCCAACATGCAAGATACCTATGAAC'TGCTTGGAAACTCCC  
 AGCTAGCTCCAAAAC'TGCAGGGACAAATCTCAGAAGAGTATAAGCAAACAGCCTTGTAAGGAAAGGCTA  
 CGCTAGTCACAGTGAGACTTACAAAAGGCTGGTTTCTTGAACATGCGTTCCAGTCCCGTGACATGTGAAC  
 ACATAGGTTTCATGCAGGTGATGATTCATAGGGTCAGAGTTCATCTCTAGAAAGTATTGCCTC  
 (SEQ ID NO:1)

FIGURE 1A

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MRPGSLLLLVLLLALSRLRGKECASPPCECHQEDDFRVTCHELHRIPSLPPSTQTLKLIETHLKTIPSLAFSSLPN  
 ISRIYLSIDATLQRLEPHSFYNLSKMTHEIRNTRSLTYIDPDALTELPLLKFLGIFNTGLRIFPDLTKIYSTDIF  
 ILEITDNPYMTSVPENAFQGLCNETLTLKLYNNGFTSVQGHAFNGTKLDAVYLNKNKYLTADNDAGGVYSGPTLL  
 DVSSTSVTALPSKGLEHLKELIAKDTWTLKKLPLSLSFLHLTRADLSYPHCCAFKNQKKIRGILESLMCNESSIRN  
 LRQRKSVNLRGPIYQEEEDPGDNSVGKQNSKFQESPSNSHYVVFEEQEDEVVGFQELKNPQETLQAFESHY  
 DYTVCGDNEDMVCTPKSDEFNPCEDIMGYRFLRIVVWFVSLALLGNIFVLLILLTSHYKLTVPFRFLMCNLAFADFC  
 MGVYLLLIASVDLYTHSEYYNHAIWQTGPGCNTAGFFTTFASELSVYTTLTVITLERWYAITFAMRLDRKIRLRHAY  
 TIMAGGWVSCFLLALLPMVGISSYAKVSICLPMDTDTPLALAYIVLVLLNVVAFVVCSCYVKIYITVRNPQYNPR  
 DKDTKIAKRAVLIFTDFMCMAPISFYALSALMNKPLITVTNSKILLVLFYPLNSCANPFLYAIFTKAFQRDVFILL  
 SKFGICKRQAQAYQGQRVCPNNSTGIQIQKIPQDTRQSLPNMQDTYELLGNSQLAPKLQGGQISEEYKQTAL  
 (SEQ ID NO:2)

FIGURE 1B

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underlined = deleted in targeting construct

[ ] = sequence flanking Neo insert in targeting construct

[CAGCGTCAGACGCAGGGCACTGAGAATGTGCGACAGCGCGCAACGATGAAGTAGCCCAG  
 AGGGTCCCTTGGAAAATGAGGCCAGGGTCCC] TGCTGCTGCTTGTCTGCTGCTCGCCCT  
GTCCAGGAGCCTGCGGGGCAAAGAGTGTGCGTCTCCACCCTGTGA [GTGTCACCAGGAGG  
 ACGACTTCAGAGTCACCTGCAAGGAGCTCCACCGAATCCCCAGCCTGCCGCCAGCACCC  
 AGACTCT] GAAGCTCATCGAGACTCATCTGAAGACCATAACCCAGTCTTGCAATTTTCGAGT  
 CTGCCCAATATTTCCAGGATCTATTTATCTATAGATGCAACTCTGCAGCGGCTGGAACCA  
 CATTCTTTCTACAATTTGAGTAAAATGACTCACATAGAAATCCGGAACACCAGAAGCTTA  
 ACCTATATAGACCCTGATGCCCTTGACAGAGCTCCCCCTTGCTCAAGTTTCTTGGCATTTC  
 AATACTGGACTTAGAATATTCCCTGACTTGACCAAAATTTATTCCACGGACATATTCTTT  
 ATACTTGAAATCACAGACAACCCCTTACATGACTTCGGTCCCTGAAAACGCATTCCAGGGC  
 CTATGCAATGAAACCTTGACCCTGAAACTGTACAACAATGGATTTACTTCAGTCCAAGGA  
 CATGCTTTCAATGGAACAAAGCTGGATGCTGTTTACCTAAACAAGAATAAATACCTGACA  
 GCTATAGACAACGATGCCCTTTGGAGGAGTATACAGTGGACCAACTTTGCTAGATGTGCTCT  
 TCCACCAGCGTCACGTGCCCTTCCTTCCAAAGGCCTGGAGCACCTCAAAGAACTGATCGCA  
 AAAGACACCTGGACTCTCAAAAAGCTCCCGCTGTCGTTGAGTTTCCTCCACCTCACTCGG  
 GCTGACCTCTCTTACCCGAGCCACTGCTGCGCTTTTAAAGAACCAGAAGAAAATCAGGGGA  
 ATCCTGGAGTCTTTGATGTGTAATGAGAGCAGTATCCGGAACCTTCGTCAAAGGAAATCA  
 GTGAACATCTTGAGGGGTCCCATCTACCAGGAATATGAAGAAGATCCGGGTGACAACAGT  
 GTTGGGTACAAACAAAACCTCCAAGTTCCAGGAGAGCCCAAGCAACTCTCACTATTACGTC  
 TTCTTTGAAGAACAAGAGGATGAGGTCGTTGGTTTCGGCCAAGAGCTCAAAAATCCTCAG  
 GAAGAGACTCTCCAAGCCTTCGAGAGCCACTATGACTACACGGTGTGTGGGGACAACGAG  
 GACATGGTGTGTACCCCAAGTCGGACGAGTTTAAACCCCTGTGAAGATATCATGGGCTAC  
 AGGTTCCCTGAGAATCGTGGTGTGGTTTGTGAGTCTGCTGGCTCTCCTGGGCAATATCTTC  
 GTCTGCTCATTCTGCTAACCAGCCACTACAAATTGACCGTGCCGCGGTTCCCTCATGTGC  
 AACTTGGCCTTTGCAGATTTCTGCATGGGGGTATACCTGCTTCTCATTGCCCTCTGTAGAC  
 CTGTACACACACTCTGAGTACTACAACCACGCCATCGACTGGCAGACGGGCCCTGGGTGC  
 AACACGGCTGGCTTCTTCACTGTTTTTCGCCAGTGAGTTATCAGTGTACACACTGACGGTC  
 ATCACCTTGAGCGATGGTACGCCATCACCTTCGCCATGCGCCTGGATAGGAAGATCCGC  
 CTCAGGCACGCGTACACCATCATGGCTGGGGGCTGGGTTTCCTGCTTCCTTCTCGCCCTG  
 CTCCCGATGGTGGGAATCAGCAGCTATGCCAAGGTCAGCATCTGCCTGCCAATGGACACC  
 GACACCCCTCTTGCACTCGCATACATTGTCTCGTTCTGCTGCTCAATGTTGTTGCCCTTT  
 GTTGTGCTGCTGTTCTGCTATGTGAAGATCTACATCACGGTCCGAAATCCCCAGTACAAC  
 CCTCGAGATAAAGACACCAAGATTGCCAAGAGGATGGCTGTGTTGATCTTCACTGACTTC  
 ATGTGCATGGCGCCCATCTCCTTCTATGCGCTGTGCGCACTTATGAACAAGCCTCTAATC  
 ACTGTTTACTAACTCCAAAATCTTGTGGTTCTCTTCTACCCCTCAACTCCTGTGCCAAT  
 CCGTTTCTCTATGCTATTTTACCAAGGCCCTTCCAGAGGGACGTGTTTCATCCTGCTCAGC  
 AAGTTTGGCATCTGCAACGCCAGGCCAGGCCATCAGGGTCAGAGAGTCTGTCCCAAC  
 AATAGCACTGGTATTCAGATCCAAAAGATTCCCCAGGACACGAGGCAGAGTCTCCCCAAC  
 ATGCAAGATACCTATGAAGTCTTGGAACTCCAGCTAGCTCCAAAACCTGCAGGGACAA  
 ATCTCAGAAGAGTATAAGCAAACAGCCTTGTAAGGAAAGGCTACGCTAGTCACAGTGAG  
 ACTTACAAAAGGCTGGTTTCTTGAACATGCGTTCCAGTCCCGTGACATGTGAACACATAG  
 GTTCATGCAGGTGATGATTCATAGGGTCAGAGTTTCATCTCTAGAAAGTATTGCCTC

FIGURE 2A

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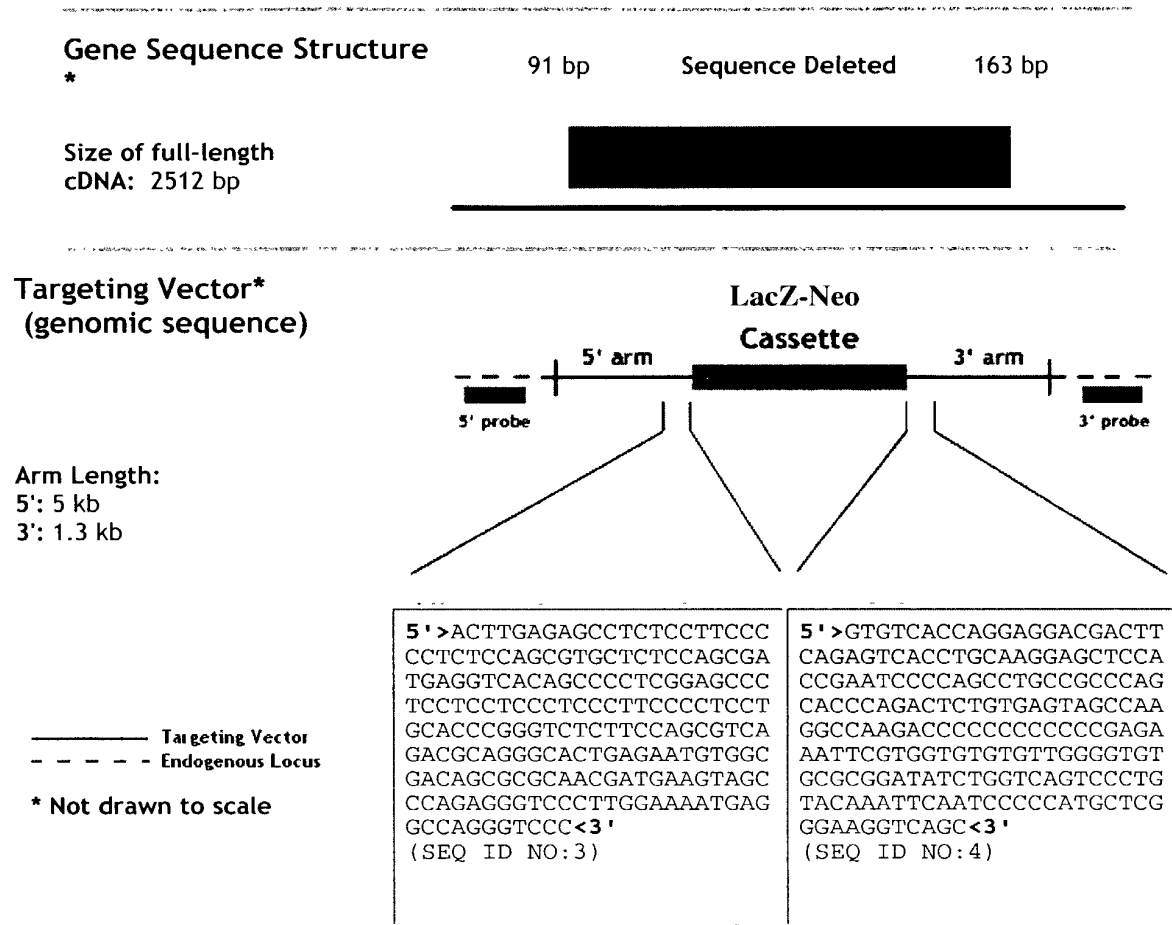


FIGURE 2B

Gender	Age (days)	Length (cm)	Body Weight (g)	Spleen/ Body Weight (g) (%)	Liver/ Body Weight (g) (%)	Kidney/ Body Weight (g) (%)	Thymus/ Body Weight (g) (%)	Heart/ Body Weight (g) (%)	Testes + Epididymis Weight (g)
+/- Female	48	10	22.339	0.095	1.256	0.327	0.082	0.155	0.694
+/- Female	48	8.25	16.960	0.052	0.307	0.220	0.060	0.122	0.719
+/- Male	48	9.5	24.550	0.069	1.388	0.342	0.055	0.224	0.485
+/- Male	48	9.7	23.792	0.081	1.192	0.304	0.063	0.133	0.559
-/- Female	48	8.5	22.619	0.080	1.272	0.238	0.080	0.121	0.535
-/- Male	48	9	24.040	0.072	1.344	0.322	0.062	0.137	0.570
-/- Female	47	7.5	9.026	0.008	0.089	0.110	0.010	0.045	0.499
-/- Female	48	7	8.360	0.016	0.191	0.110	0.004	0.051	0.610
-/- Female	48	8	11.640	0.016	0.137	0.127	0.031	0.266	0.455
-/- Male	48	7.6	11.733	0.018	0.153	0.134	0.034	0.290	0.452
-/- Male	48	8	12.545	0.024	0.191	0.146	0.035	0.060	0.478
-/- Male	48	7	8.070	0.007	0.087	0.095	0.001	0.042	0.520

FIGURE 3

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Gender	Age at Test (days)	Spleen/			Liver/			Kidney/			Thymus/			Heart/			Testes + Epididymis Weight (g)
		Body Weight (g)	Spleen Weight (g)	Spleen (%)	Body Weight (g)	Liver Weight (g)	Liver (%)	Body Weight (g)	Kidney Weight (g)	Kidney (%)	Thymus Weight (g)	Thymus (%)	Body Weight (g)	Heart Weight (g)	Heart (%)		
+/-	Female	308	9.5	25.191	0.222	0.8813	1.476	5.8592	0.353	1.4013	0.039	0.1548	0.145	0.5756			
+/-	Female	308	9.18	28.180	0.091	0.3229	1.447	5.1348	0.383	1.3591	0.043	0.1526	0.136	0.4826			
+/-	Male	308	11.025	55.089	0.182	0.3304	3.267	5.9304	0.694	1.2598	0.074	0.1343	0.219	0.3975		0.35	
+/-	Male	308	11	42.613	0.136	0.3192	2.144	5.0313	0.485	1.1382	0.052	0.1220	0.201	0.4717		0.387	
-/-	Female	307	7.978	19.561	0.030	0.1534	0.863	4.4118	0.184	0.9406	0.040	0.2045	0.109	0.5572			
-/-	Male	307	9.47	25.557	0.077	0.3013	1.394	5.4545	0.340	1.3304	0.025	0.0978	0.111	0.4343		0.401	
-/-	Male	307	9.5	25.263	0.051	0.2019	1.232	4.8767	0.296	1.1717	0.027	0.1069	0.102	0.4038		0.389	

**FIGURE 4**

[illegible]